

CRF Errors Corrected by the STIC Systems Branch

CRF Processing Date:

4/11/2001

OIPF #B

Serial Number: 09/757,1003

ENTERED

Edited by:

Verified by:

(STIC staff)

Changed a file from non-ASCII to ASCII

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

Edited a format error in the Current Application Data section, specifically:

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____

Added the mandatory heading and subheadings for "Current Application Data".

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included:

Deleted extra, invalid, headings used by an applicant, specifically:

Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file;
 page numbers throughout text; other invalid text, such as _____

Inserted mandatory headings, specifically:

Corrected an obvious error in the response, specifically:

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically:

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted

Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected:

Other: Seq 2 - corrected amino acid nos.

DRAFT

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/757,100B

DATE: 04/11/2001

TIME: 15:26:09

Input Set : A:\Isph-533.txt
 Output Set: N:\CRF3\04112001\I757100B.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: Monia, Brett P.
 4 Gaarde, William A.
 5 Nero, Pamela S.
 8 <120> TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase
 9 Expression
 11 <130> FILE REFERENCE: ISPH-0533
 13 <140> CURRENT APPLICATION NUMBER: US/09/757,100B
 C--> 14 <141> CURRENT FILING DATE: 2001-03-15
 16 <150> PRIOR APPLICATION NUMBER: 09/377,310
 17 <151> PRIOR FILING DATE: 1999-08-19
 19 <150> PRIOR APPLICATION NUMBER: PCT/US00/18999
 20 <151> PRIOR FILING DATE: 2000-07-13
 22 <160> NUMBER OF SEQ ID NOS: 44
 24 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

337 <210> SEQ ID NO: 2
 338 <211> LENGTH: 1052
 339 <212> TYPE: PRT
 340 <213> ORGANISM: Homo sapiens
 342 <400> SEQUENCE: 2
 343 Met Ala Ala Ala Tyr Leu Asp Pro Asn Leu Asn His Thr Pro Asn Ser
 344 1 5 10 15
 346 Ser Thr Lys Thr His Leu Gly Thr Gly Met Glu Arg Ser Pro Gly Ala
 347 20 25 30
 349 Met Glu Arg Val Leu Lys Val Phe His Tyr Phe Glu Ser Asn Ser Glu
 350 35 40 45
 352 Pro Thr Thr Trp Ala Ser Ile Ile Arg His Gly Asp Ala Thr Asp Val
 353 50 55 60
 355 Arg Gly Ile Ile Gln Lys Ile Val Asp Ser His Lys Val Lys His Val
 356 65 70 75 80
 358 Ala Cys Tyr Gly Phe Arg Leu Ser His Leu Arg Ser Glu Glu Val His
 359 85 90 95
 361 Trp Leu His Val Asp Met Gly Val Ser Ser Val Arg Glu Lys Tyr Glu
 362 100 105 110
 364 Leu Ala His Pro Pro Glu Glu Trp Lys Tyr Glu Leu Arg Ile Arg Tyr
 365 115 120 125
 367 Leu Pro Lys Gly Phe Leu Asn Gln Phe Thr Glu Asp Lys Pro Thr Leu
 368 130 135 140
 370 Asn Phe Phe Tyr Gln Gln Val Lys Ser Asp Tyr Met Leu Glu Ile Ala
 371 145 150 155 160
 373 Asp Gln Val Asp Gln Glu Ile Ala Leu Lys Leu Gly Cys Leu Glu Ile
 374 165 170 175
 376 Arg Arg Ser Tyr Trp Glu Met Arg Gly Asn Ala Leu Glu Lys Lys Ser
 377 180 185 190

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379 Asn Tyr Glu Val Leu Glu Lys Asp Val Gly Leu Lys Arg Phe Phe Pro
 380 195 200 205
 382 Lys Ser Leu Leu Asp Ser Val Lys Ala Lys Thr Leu Arg Lys Leu Ile
 383 210 215 220
 385 Gln Gln Thr Phe Arg Gln Phe Ala Asn Leu Asn Arg Glu Glu Ser Ile
 386 225 230 235 240
 388 Leu Lys Phe Phe Glu Ile Leu Ser Pro Val Tyr Arg Phe Asp Lys Glu
 389 245 250 255
 391 Cys Phe Lys Cys Ala Leu Gly Ser Ser Trp Ile Ile Ser Val Glu Leu
 392 260 265 270
 394 Ala Ile Gly Pro Glu Glu Gly Ile Ser Tyr Leu Thr Asp Lys Gly Cys
 395 275 280 285
 398 Asn Pro Thr His Leu Ala Asp Phe Thr Gln Val Gln Thr Ile Gln Tyr
 399 290 295 300
 401 Ser Asn Ser Glu Asp Lys Asp Arg Lys Gly Met Leu Gln Leu Lys Ile
 402 305 310 315 320
 404 Ala Gly Ala Pro Glu Pro Leu Thr Val Thr Ala Pro Ser Leu Thr Ile
 405 325 330 335
 407 Ala Glu Asn Met Ala Asp Leu Ile Asp Gly Tyr Cys Arg Leu Val Asn
 408 340 345 350
 410 Gly Thr Ser Gln Ser Phe Ile Ile Arg Pro Gln Lys Glu Gly Glu Arg
 411 355 360 365
 413 Ala Leu Pro Ser Ile Pro Lys Leu Ala Asn Ser Glu Lys Gln Gly Met
 414 370 375 380
 416 Arg Thr His Ala Val Ser Val Ser Glu Thr Asp Asp Tyr Ala Glu Ile
 417 385 390 395 400
 419 Ile Asp Glu Glu Asp Thr Tyr Thr Met Pro Ser Thr Arg Asp Tyr Glu
 420 405 410 415
 422 Ile Gln Arg Glu Arg Ile Glu Leu Gly Arg Cys Ile Gly Glu Gly Gln
 423 420 425 430
 425 Phe Gly Asp Val His Gln Gly Ile Tyr Met Ser Pro Glu Asn Pro Ala
 426 435 440 445
 428 Leu Ala Val Ala Ile Lys Thr Cys Lys Asn Cys Thr Ser Asp Ser Val
 429 450 455 460
 431 Arg Glu Lys Phe Leu Gln Glu Ala Leu Thr Met Arg Gln Phe Asp His
 432 465 470 475 480
 434 Pro His Ile Val Lys Leu Ile Gly Val Ile Thr Glu Asn Pro Val Trp
 435 485 490 495
 437 Ile Ile Met Glu Leu Cys Thr Leu Gly Glu Leu Arg Ser Phe Leu Gln
 438 500 505 510
 440 Val Arg Lys Tyr Ser Leu Asp Leu Ala Ser Leu Ile Leu Tyr Ala Tyr
 441 515 520 525
 443 Gln Leu Ser Thr Ala Leu Ala Tyr Leu Glu Ser Lys Arg Phe Val His
 444 530 535 540
 446 Arg Asp Ile Ala Ala Arg Asn Val Leu Val Ser Ser Asn Asp Cys Val
 447 545 550 555 560
 449 Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Met Glu Asp Ser Thr Tyr
 450 565 570 575
 452 Tyr Lys Ala Ser Lys Gly Lys Leu Pro Ile Lys Trp Met Ala Pro Glu

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453	580	585	590
455	Ser Ile Asn Phe Arg Arg Phe Thr Ser Ala Ser Asp Val Trp Met Phe		
456	595	600	605
458	Gly Val Cys Met Trp Glu Ile Leu Met His Gly Val Lys Pro Phe Gln		
459	610.	615	620
461	Gly Val Lys Asn Asn Asp Val Ile Gly Arg Ile Glu Asn Gly Glu Arg		
462	625	630	635
464	Leu Pro Met Pro Pro Asn Cys Pro Pro Thr Leu Tyr Ser Leu Met Thr		
465	645	650	655
467	Lys Cys Trp Ala Tyr Asp Pro Ser Arg Arg Pro Arg Phe Thr Glu Leu		
468	660	665	670
470	Lys Ala Gln Leu Ser Thr Ile Leu Glu Glu Lys Ala Gln Gln Glu		
471	675	680	685
473	Glu Arg Met Arg Met Glu Ser Arg Arg Gln Ala Thr Val Ser Trp Asp		
474	690	695	700
476	Ser Gly Gly Ser Asp Glu Ala Pro Pro Lys Pro Ser Arg Pro Gly Tyr		
477	705	710	715
479	Pro Ser Pro Arg Ser Ser Glu Gly Phe Tyr Pro Ser Pro Gln His Met		
480	725	730	735
482	Val Gln Thr Asn His Tyr Gln Val Ser Gly Tyr Pro Gly Ser His Gly		
483	740	745	750
485	Ile Thr Ala Met Ala Gly Ser Ile Tyr Pro Gly Gln Ala Ser Leu Leu		
486	755	760	765
488	Asp Gln Thr Asp Ser Trp Asn His Arg Pro Gln Glu Ile Ala Met Trp		
489	770	775	780
491	Gln Pro Asn Val Glu Asp Ser Thr Val Leu Asp Leu Arg Gly Ile Gly		
492	785	790	795
494	Gln Val Leu Pro Thr His Leu Met Glu Glu Arg Leu Ile Arg Gln Gln		
495	805	810	815
497	Gln Glu Met Glu Glu Asp Gln Arg Trp Leu Glu Lys Glu Glu Arg Phe		
498	820	825	830
500	Leu Lys Pro Asp Val Arg Leu Ser Arg Gly Ser Ile Asp Arg Glu Asp		
501	835	840	845
503	Gly Ser Leu Gln Gly Pro Ile Gly Asn Gln His Ile Tyr Gln Pro Val		
504	850	855	860
506	Gly Lys Pro Asp Pro Ala Ala Pro Pro Lys Lys Pro Pro Arg Pro Gly		
507	865	870	875
509	Ala Pro Gly His Leu Gly Ser Leu Ala Ser Leu Ser Ser Pro Ala Asp		
510	885	890	895
512	Ser Tyr Asn Glu Gly Val Lys Leu Gln Pro Gln Glu Ile Ser Pro Pro		
513	900	905	910
515	Pro Thr Ala Asn Leu Asp Arg Ser Asn Asp Lys Val Tyr Glu Asn Val		
516	915	920	925
518	Thr Gly Leu Val Lys Ala Val Ile Glu Met Ser Ser Lys Ile Gln Pro		
519	930	935	940
521	Ala Pro Pro Glu Glu Tyr Val Pro Met Val Lys Glu Val Gly Leu Ala		
522	945	950	955
524	Leu Arg Thr Leu Leu Ala Thr Val Asp Glu Thr Ile Pro Leu Leu Pro		
525	965	970	975

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527 Ala Ser Thr His Arg Glu Ile Glu Met Ala Gln Lys Leu Leu Asn Ser
528 980 985 990
530 Asp Leu Gly Glu Leu Ile Asn Lys Met Lys Leu Ala Gln Gln Tyr Val
531 995 1000 1005
533 Met Thr Ser Leu Gln Gln Glu Tyr Lys Lys Gln Met Leu Thr Ala Ala
534 1010 1015 1020
536 His Ala Leu Ala Val Asp Ala Lys Asn Leu Leu Asp Val Ile Asp Gln
E--> 537 025 1025 1030 1035 1040
539 Ala Arg Leu Lys Met Leu Gly Gln Thr Arg Pro His
540 1045 1050
1033 <210> SEQ ID NO: 44
1034 <211> LENGTH: 20
1035 <212> TYPE: DNA
1036 <213> ORGANISM: Artificial Sequence
1038 <220> FEATURE:
1039 <223> OTHER INFORMATION: control sequence
1041 <220> FEATURE:
1042 <221> NAME/KEY: unsure
1043 <222> LOCATION: (1)..(20)
1045 <400> SEQUENCE: 44
W--> 1046 nnnnnnnnnnnnnnnnn
E--> 1050 17

20

VERIFICATION SUMMARY DATE: 04/11/2001
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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:537 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:1046 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44
L:1050 M:254 E: No. of Bases conflict, LENGTH:Input:17 Counted:20 SEQ:44